S. Unser
1642
/3

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/234,290*

DATE: 04/11/2000
TIME: 20:32:46

INPUT SET: S35250.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                          SEQUENCE LISTING          ENTERED
 2
 3   (1)      General Information
 4
 5            (i) APPLICANT: Burkly, Linda C.
 6
 7            (ii) TITLE OF THE INVENTION: TREATMENT FOR INSULIN DEPENDENT
 8                     DIABETES
 9
10            (iii) NUMBER OF SEQUENCES: 16
11
12            (iv) CORRESPONDENCE ADDRESS:
13               (A) ADDRESSEE: Fish & Richardson P.C.
14               (B) STREET: 225 Franklin Street
15               (C) CITY: Boston
16               (D) STATE: MA
17               (E) COUNTRY: USA
18               (F) ZIP: 02110-2804
19
20            (v) COMPUTER READABLE FORM:
21               (A) MEDIUM TYPE: Diskette
22               (B) COMPUTER: IBM Compatible
23               (C) OPERATING SYSTEM: DOS
24               (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26            (vi) CURRENT APPLICATION DATA:
27               (A) APPLICATION NUMBER: 09/234,290
28               (B) FILING DATE: 20-JAN-1999
29
30            (vii) PRIOR APPLICATION DATA:
31               (A) APPLICATION NUMBER: 08/447,118
32               (B) FILING DATE: 22-MAY-1995
33
34               (A) APPLICATION NUMBER: PCT/US94/01456
35               (B) FILING DATE: 09-FEB-1994
36
37               (A) APPLICATION NUMBER: 08/029,330
38               (B) FILING DATE: 09-FEB-1993
39
40            (viii) ATTORNEY/AGENT INFORMATION:
41               (A) NAME: Myers, Louis
42               (B) REGISTRATION NUMBER: 35,965
43               (C) REFERENCE/DOCKET NUMBER: 10274/008003
44
45            (ix) TELECOMMUNICATION INFORMATION:
46               (A) TELEPHONE: 617/542-5070
```

```
47            (B)  TELEFAX: 617/542-8906
48
49
50            (2)  INFORMATION FOR SEQ ID NO:1:
51
52         (i) SEQUENCE CHARACTERISTICS:
53            (A)  LENGTH: 360 base pairs
54            (B)  TYPE: nucleic acid
55            (C)  STRANDEDNESS: single
56            (D)  TOPOLOGY: linear
57
58         (ix) FEATURE:
59            (A)  NAME/KEY: Coding Sequence
60            (B)  LOCATION: 1...360
61
62         (ix) FEATURE:
63            (A)  NAME/KEY: misc_feature
64            (B)  LOCATION: 1
65            (D)  OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
66                     chain variable region; amino acid 1 is Glu (E) but
67                     Gln (Q) may be substituted"
68
69         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71      GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA        48
72      Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
73       1           5                   10                  15
74
75      GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT        96
76      Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
77                  20                  25                  30
78
79      ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA       144
80      Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
81          35                  40                  45
82
83      AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG       192
84      Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
85          50                  55                  60
86
87      GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG       240
88      Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
89       65                  70                  75                  80
90
91      CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA       288
92      Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
93                  85                  90                  95
94
95      GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA       336
96      Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
97                  100                 105                 110
98
99      GGG ACC ACG GTC ACC GTC TCC TCA                                      360·
```

INPUT SET: S35250.raw

```
100     Gly Thr Thr Val Thr Val Ser Ser
101         115             120
102
103             (2) INFORMATION FOR SEQ ID NO:2:
104
105         (i) SEQUENCE CHARACTERISTICS:
106             (A) LENGTH: 120 amino acids
107             (B) TYPE: amino acid
108             (D) TOPOLOGY: linear
109
110         (ii) MOLECULE TYPE: protein
111
112         (v) FRAGMENT TYPE: internal
113
114         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116     Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
117      1               5                  10                  15
118     Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
119              20                  25                  30
120     Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
121          35                  40                  45
122     Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
123          50                  55                  60
124     Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
125      65                  70                  75                  80
126     Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
127              85                  90                  95
128     Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
129              100                 105                 110
130     Gly Thr Thr Val Thr Val Ser Ser
131         115             120
132
133             (2) INFORMATION FOR SEQ ID NO:3:
134
135         (i) SEQUENCE CHARACTERISTICS:
136             (A) LENGTH: 318 base pairs
137             (B) TYPE: nucleic acid
138             (C) STRANDEDNESS: single
139             (D) TOPOLOGY: linear
140
141         (ii) MOLECULE TYPE: cDNA
142
143         (ix) FEATURE:
144             (A) NAME/KEY: Coding Sequence
145             (B) LOCATION: 1...318
146             (D) OTHER INFORMATION:/product= "HP1/2 light chain
147                 variable region"
148
149         (ix) FEATURE:
150             (A) NAME/KEY: misc_feature
151             (B) LOCATION: 1
152             (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2
```

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/234,290

DATE: 04/11/2000
TIME: 20:32:47

INPUT SET: S35250.raw

```
153                          light chain variable region"
154
155             (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:3:
156
157     AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA          48
158     Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
159      1               5                  10                  15
160
161     GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT          96
162     Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
163                  20                  25                  30
164
165     GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA         144
166     Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
167              35  .                  40                  45
168
169     TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC         192
170     Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
171          50                  55                  60
172
173     AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT         240
174     Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
175      65                  70                  75                  80
176
177     GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC         288
178     Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
179                  85                  90                  95
180
181     ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC                               318
182     Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
183              100                 105
184
185             (2)  INFORMATION FOR SEQ ID NO:4:
186
187          (i)  SEQUENCE CHARACTERISTICS:
188             (A)  LENGTH: 106 amino acids  .
189             (B)  TYPE: amino acid
190             (D)  TOPOLOGY: linear
191
192          (ii)  MOLECULE TYPE: protein
193
194          (v)  FRAGMENT TYPE: internal
195
196          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
197
198     Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
199      1               5                  10                  15
200     Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
201                  20                  25                  30
202     Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
203              35                  40                  45
204     Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
205          50                  55                  60
```

INPUT SET: S35250.raw

```
206    Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
207     65                  70              75                  80
208    Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
209                     85              90                  95
210    Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
211                100              105
212
213            (2) INFORMATION FOR SEQ ID NO:5:
214
215            (i) SEQUENCE CHARACTERISTICS:
216              (A) LENGTH: 429 base pairs
217              (B) TYPE: nucleic acid
218              (C) STRANDEDNESS: single
219              (D) TOPOLOGY: linear
220
221            (ii) MOLECULE TYPE: cDNA
222
223            (ix) FEATURE:
224              (A) NAME/KEY: Coding Sequence
225              (B) LOCATION: 1...429
226
227            (ix) FEATURE:
228              (A) NAME/KEY: sig_peptide
229              (B) LOCATION: 1...57
230
231            (ix) FEATURE:
232              (A) NAME/KEY: mat_peptide
233              (B) LOCATION: 58...429
234
235            (ix) FEATURE:
236              (A) NAME/KEY: misc_feature
237              (B) LOCATION: 1
238              (D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy
239                   chain variable region"
240
241            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
242
243    ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT        48
244    Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
245    -19              -15              -10                  -5
246
247    GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA        96
248    Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
249                 1               5                  10
250
25
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/234,290*

INPUT SET: S35250.raw

Line   Error   Original Text